

# SEQUENCE LISTING

<110> Mitsubishi Chemical Corporation

<120> A protein which is involved in recovery of cytoplasm male fertility from sterility and a gene encoding the protein

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 Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val  
 65 70 75 80  
 Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp  
 85 90 95  
 Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Arg Cys  
 100 105 110  
 Asp Ile Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser  
 115 120 125  
 Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Ile Thr Lys Leu Gly  
 130 135 140  
 Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly Leu Cys  
 145 150 155 160  
 Val Glu Asp Arg Val Ser Glu Ala Leu Asp Phe Phe His Gln Met Phe  
 165 170 175  
 Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu Met Asn  
 180 185 190  
 Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu Leu Asp  
 195 200 205  
 Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr  
 210 215 220  
 Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn  
 225 230 235 240  
 Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val

	245	250	255
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser			
	260	265	270
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro			
	275	280	285
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly			
	290	295	300
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys			
305	310	315	320
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val			
	325	330	335
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu			
	340	345	350
Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp			
	355	360	365
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr			
	370	375	380
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr			
385	390	395	400
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu			
	405	410	415
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr			
	420	425	430
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala			
	435	440	445
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp			
	450	455	460

Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys			
465	470	475	480
Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys			
	485	490	495
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln			
	500	505	510
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu			
	515	520	525
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro			
	530	535	540
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser			
545	550	555	560
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser			
	565	570	575
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys			
	580	585	590
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly			
	595	600	605
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys			
	610	615	620
Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln			
625	630	635	640
Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn			
	645	650	655
Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala			
	660	665	670
Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly			

	675	680	685
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<211>	25		
<212>	DNA		
<213>	Artificial Sequence		
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<400>	4		
	gaagcaaaaa agaaaacgag cagag		25
<210>	5		
<211>	25		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Description of Artificial Sequence: Synthetic DNA		
<400>	5		
	ccaaaaatcc gaaatccgaa tagac		25
<210>	6		
<211>	20		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Description of Artificial Sequence: Synthetic DNA		
<400>	6		
	ctcggctctg ggtttagtga		20
<210>	7		
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 7

tccacaaacc ctagccaaca 20

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 8

gcttatgctt ctctggttcg cctc 24

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

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ctcagttttc gtcaccttac acaatgc 27

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: Synthetic DNA

<400> 10

gattcctttc tcttgcatTT cag 23

<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 11

atctcgtcct ttaccttctg tgg 23

<210> 12

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 12

cgggatccgc tcacaatt 18

<210> 13

<211> 100

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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gcggatccca atttcattct gcatcactct ccctgtcgtt atcgacctcg caaggttttt 60

gaaacggccg aaacgggaag tgacaatacc gcttttcttc 100

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<211> 100

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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cgaaaaaggt aatcatgcat ttatatgctg aagaaaagcg 100

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<211> 3306

<212> DNA

<213> Raphanus sativus

<400> 15

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ggattcagtt tttttgtcca gccctactct gaacagtaga taaaaaatag aaccctaaat 120

taataggtta gattttgggt aggtctttct aattagtatg gagattctcg attccttctc 180

attgcagtgt ggtatgtcca actcattggt tatgtacata tccaatttag ttttgagtca 240

aatgttttagt tacttaagag ttgaatgaaa taggggatga tattgatggc caaggttctc 300

ccaaagtaaa taactttggt tatattttta gttagcttat aacatcaata aaaatgtcat 360

taactgggtc aataaaaatg tcattaactg gttcctctaa tataattatt taacacacct 420

ggctgttgat aaatttttat gatcgtttaa taattttaga agtggatagt ctgtaaatgg 480

tctttgattg gtcgtcttga tttttaaaag tggactaaac aagaaggctt agtaataaat 540

actgaaccgg aactctactg gtttcaatag ctcggtttat caatttctct cggtcttggg 600

tttagtgaat catgtggccc tgtgggttta aacaaggaac tcaatcaatc aactggtgac 660

aaatctgaac cggaatttgt ataattcaaa ctgaaccggt tcttgtaaaa caaatggaac 720

ccgtttgtac tttatctctc gtttattttc tcagtcacga gtttttttta gagatcgacg 780  
 aagaacaaaa tttaggcgaa acaaaaaataa aatgttggct agggtttgtg gattcaagtg 840  
 ttctttcttct cctgctgagt ctgcggctag attgttctgt acgagatcga ttcgtgatac 900  
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 taagaaggga gatactgtgt ctgcactgaa tctgctgagg aagatggagg aggtgagcca 1560  
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tgttcaaact tacaatatat tgatcagcgg cttgatcaat gaaggggaagt ttttagaggc 2400  
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<211> 2064

<212> DNA

<213> Raphanus sativus

<400> 16

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Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Glu

1 5 10 15

tct gcg gct aga ttg ttc tgt acg aga tcg att cgt gat act ctg gcc 96

Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala

20	25	30	
aag gca agc gga gag agt tgc gaa gca ggt ttt gga gga gag agt ttg	144		
Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu			
35	40	45	
aag ctg caa agt ggg ttt cat gaa atc aaa ggt tta gag gat gcg att	192		
Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile			
50	55	60	
gat ttg ttc agt gac atg ctt cga tct cgt cct tta cct tct gtg gtt	240		
Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val			
65	70	75	80
gat ttc tgt aaa ttg atg ggt gtg gtg gtg aga atg gaa cgc ccg gat	288		
Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp			
85	90	95	
ctt gtg att tct ctc tat cag aag atg gaa agg aaa cag att cga tgt	336		
Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Arg Cys			
100	105	110	
gat ata tac agc ttc aat att ctg ata aaa tgt ttc tgc agc tgc tct	384		
Asp Ile Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser			
115	120	125	
aag ctc ccc ttt gct ttg tct aca ttt ggt aag ctc acc aag ctt gga	432		
Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys Leu Gly			
130	135	140	
ctc cac cct gat gtt gtt acc ttc acc acc ctg ctc cac gga ttg tgc	480		
Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly Leu Cys			
145	150	155	160
gtg gaa gat agg gtt tct gaa gct ttg aat ttg ttt cat caa atg ttt	528		
Val Glu Asp Arg Val Ser Glu Ala Leu Asn Leu Phe His Gln Met Phe			

165	170	175	
gaa acg aca tgt agg ccc aat gtc gta acc ttc acc act ttg atg aac		576	
Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu Met Asn			
180	185	190	
ggt ctt tgc cgc gag ggt aga att gtc gaa gcc gta gct ctg ctt gat		624	
Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu Leu Asp			
195	200	205	
cgg atg atg gaa gat ggt ctc cag cct acc cag att act tat gga aca		672	
Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr Gly Thr			
210	215	220	
atc gta gat ggg atg tgt aag aag gga gat act gtg tct gca ctg aat		720	
Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala Leu Asn			
225	230	235	240
ctg ctg agg aag atg gag gag gtg agc cac atc ata ccc aat gtt gta		768	
Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn Val Val			
245	250	255	
atc tat agt gca atc att gat agc ctt tgt aaa gac gga cgt cat agc		816	
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser			
260	265	270	
gat gca caa aat ctt ttc act gaa atg caa gag aaa gga atc ttt ccc		864	
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro			
275	280	285	
gat tta ttt acc tac aac agt atg ata gtt ggt ttt tgt agc tct ggt		912	
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly			
290	295	300	
aga tgg agc gac gcg gag cag ttg ttg caa gaa atg tta gaa agg aag		960	
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys			

305	310	315	320
atc agc cct gat gtt gta act tat aat gct ttg atc aat gca ttt gtc 1008			
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val			
325	330	335	
aag gaa ggc aag ttc ttt gag gct gaa gaa tta tac gat gag atg ctt 1056			
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu			
340	345	350	
cca agg ggt ata atc cct aat aca atc aca tat agt tca atg atc gat 1104			
Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp			
355	360	365	
gga ttt tgc aaa cag aat cgt ctt gat gct gct gag cac atg ttt tat 1152			
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr			
370	375	380	
ttg atg gct acc aag ggc tgc tct ccc aac cta atc act ttc aat act 1200			
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr			
385	390	395	400
ctc ata gac gga tat tgt ggg gct aag agg ata gat gat gga atg gaa 1248			
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu			
405	410	415	
ctt ctc cat gag atg act gaa aca gga tta gtt gct gac aca act act 1296			
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr			
420	425	430	
tac aac act ctt att cac ggg ttc tat ctg gtg ggc gat ctt aat gct 1344			
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala			
435	440	445	
gct cta gac ctt tta caa gag atg atc tct agt ggt ttg tgc cct gat 1392			
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp			

450	455	460	
atc gtt act tgt gac act ttg ctg gat ggt ctc tgc gat aat ggg aaa 1440			
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465	470	475	480
cta aaa gat gca ttg gaa atg ttt aag gtt atg cag aag agt aag aag 1488			
Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys			
	485	490	495
gat ctt gat gct agt cac ccc ttc aat ggt gtg gaa cct gat gtt caa 1536			
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln			
	500	505	510
act tac aat ata ttg atc agc ggc ttg atc aat gaa ggg aag ttt tta 1584			
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu			
	515	520	525
gag gcc gag gaa tta tac gag gag atg ccc cac agg ggt ata gtc cca 1632			
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro			
530	535	540	
gat act atc acc tat agc tca atg atc gat gga tta tgc aag cag agc 1680			
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser			
545	550	555	560
cgc cta gat gag gct aca caa atg ttt gat tcg atg ggt agc aag agc 1728			
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser			
	565	570	575
ttc tct cca aac gta gtg acc ttt act aca ctc att aat ggc tac tgt 1776			
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys			
	580	585	590
aag gca gga agg gtt gat gat ggg ctg gag ctt ttc tgc gag atg ggt 1824			
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly			



595	600	605	
cga aga ggg ata gtt gct aac gca att act tac atc act ttg att tgt	1872		
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys			
610	615	620	
ggt ttt cgt aaa gtg ggt aat att aat ggg gct cta gac att ttc cag	1920		
Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln			
625	630	635	640
gag atg att tca agt ggt gtg tat cct gat acc att acc atc cgc aat	1968		
Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn			
645	650	655	
atg ctg act ggt tta tgg agt aaa gag gaa cta aaa agg gca gtg gca	2016		
Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala			
660	665	670	
atg ctt gag aaa ctg cag atg agt atg gat cta tca ttt ggg gga tga	2064		
Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly Xaa			
675	680	685	
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<213> Raphanus sativus			
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1	5	10	15
Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala			
20	25	30	
Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu			
35	40	45	

Lys	Leu	Gln	Ser	Gly	Phe	His	Glu	Ile	Lys	Gly	Leu	Glu	Asp	Ala	Ile
50									55						60
Asp	Leu	Phe	Ser	Asp	Met	Leu	Arg	Ser	Arg	Pro	Leu	Pro	Ser	Val	Val
65						70					75				80
Asp	Phe	Cys	Lys	Leu	Met	Gly	Val	Val	Val	Arg	Met	Glu	Arg	Pro	Asp
						85				90					95
Leu	Val	Ile	Ser	Leu	Tyr	Gln	Lys	Met	Glu	Arg	Lys	Gln	Ile	Arg	Cys
						100				105					110
Asp	Ile	Tyr	Ser	Phe	Asn	Ile	Leu	Ile	Lys	Cys	Phe	Cys	Ser	Cys	Ser
						115				120					125
Lys	Leu	Pro	Phe	Ala	Leu	Ser	Thr	Phe	Gly	Lys	Leu	Thr	Lys	Leu	Gly
						130				135					140
Leu	His	Pro	Asp	Val	Val	Thr	Phe	Thr	Thr	Leu	Leu	His	Gly	Leu	Cys
145						150				155					160
Val	Glu	Asp	Arg	Val	Ser	Glu	Ala	Leu	Asn	Leu	Phe	His	Gln	Met	Phe
						165				170					175
Glu	Thr	Thr	Cys	Arg	Pro	Asn	Val	Val	Thr	Phe	Thr	Thr	Leu	Met	Asn
						180				185					190
Gly	Leu	Cys	Arg	Glu	Gly	Arg	Ile	Val	Glu	Ala	Val	Ala	Leu	Leu	Asp
						195				200					205
Arg	Met	Met	Glu	Asp	Gly	Leu	Gln	Pro	Thr	Gln	Ile	Thr	Tyr	Gly	Thr
						210				215					220
Ile	Val	Asp	Gly	Met	Cys	Lys	Lys	Gly	Asp	Thr	Val	Ser	Ala	Leu	Asn
225						230				235					240
Leu	Leu	Arg	Lys	Met	Glu	Glu	Val	Ser	His	Ile	Ile	Pro	Asn	Val	Val
						245				250					255
Ile	Tyr	Ser	Ala	Ile	Ile	Asp	Ser	Leu	Cys	Lys	Asp	Gly	Arg	His	Ser

	260		265		270										
Asp	Ala	Gln	Asn	Leu	Phe	Thr	Glu	Met	Gln	Glu	Lys	Gly	Ile	Phe	Pro
	275		280		285										
Asp	Leu	Phe	Thr	Tyr	Asn	Ser	Met	Ile	Val	Gly	Phe	Cys	Ser	Ser	Gly
	290		295		300										
Arg	Trp	Ser	Asp	Ala	Glu	Gln	Leu	Leu	Gln	Glu	Met	Leu	Glu	Arg	Lys
305			310		315									320	
Ile	Ser	Pro	Asp	Val	Val	Thr	Tyr	Asn	Ala	Leu	Ile	Asn	Ala	Phe	Val
			325		330									335	
Lys	Glu	Gly	Lys	Phe	Phe	Glu	Ala	Glu	Glu	Leu	Tyr	Asp	Glu	Met	Leu
	340		345		350										
Pro	Arg	Gly	Ile	Ile	Pro	Asn	Thr	Ile	Thr	Tyr	Ser	Ser	Met	Ile	Asp
	355		360		365										
Gly	Phe	Cys	Lys	Gln	Asn	Arg	Leu	Asp	Ala	Ala	Glu	His	Met	Phe	Tyr
	370		375		380										
Leu	Met	Ala	Thr	Lys	Gly	Cys	Ser	Pro	Asn	Leu	Ile	Thr	Phe	Asn	Thr
385			390		395									400	
Leu	Ile	Asp	Gly	Tyr	Cys	Gly	Ala	Lys	Arg	Ile	Asp	Asp	Gly	Met	Glu
			405		410									415	
Leu	Leu	His	Glu	Met	Thr	Glu	Thr	Gly	Leu	Val	Ala	Asp	Thr	Thr	Thr
	420		425		430										
Tyr	Asn	Thr	Leu	Ile	His	Gly	Phe	Tyr	Leu	Val	Gly	Asp	Leu	Asn	Ala
	435		440		445										
Ala	Leu	Asp	Leu	Leu	Gln	Glu	Met	Ile	Ser	Ser	Gly	Leu	Cys	Pro	Asp
	450		455		460										
Ile	Val	Thr	Cys	Asp	Thr	Leu	Leu	Asp	Gly	Leu	Cys	Asp	Asn	Gly	Lys
465			470		475									480	

Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys			
485	490	495	
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln			
500	505	510	
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu			
515	520	525	
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro			
530	535	540	
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser			
545	550	555	560
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser			
565	570	575	
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys			
580	585	590	
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly			
595	600	605	
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys			
610	615	620	
Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln			
625	630	635	640
Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn			
645	650	655	
Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala			
660	665	670	
Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly Xaa			
675	680	685	

<210> 18

<211> 2073

<212> DNA

<213> Raphanus sativus

<400> 18

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tct gcg gct aga ttg ttc tgt acg aga tcg att cgt gat act ctg gcc 96
Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala
              20              25              30
aag gca agc agg gat gga gag agt tgc gaa gca ggt ttt gga gga gag 144
Lys Ala Ser Arg Asp Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu
              35              40              45
agt ttg aag ctg caa agt ggg ttt cat gaa atc aaa ggt tta gag gat 192
Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp
              50              55              60
gcg att gat ttg ttc agt gac atg ctt cga tct cgt cct tta cct tct 240
Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser
      65              70              75              80
gtg gtt gat ttc tgt aaa ttg atg ggt gtg gtg gtg agg atg aaa cgc 288
Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Lys Arg
              85              90              95
ccg gat gtt gtg att tct ctc cat aag aag atg gaa atg cgg cgc att 336
Pro Asp Val Val Ile Ser Leu His Lys Lys Met Glu Met Arg Arg Ile
              100              105              110
cca tgt gat gca tac agc ttc aat att ctg ata aag tgt ttc tgc agc 384
Pro Cys Asp Ala Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser
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115	120	125	
tgc tct aag ctg ccc ttt gct ttg tct aca ttt ggt aag ctc acc aag	432		
Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys			
130	135	140	
ctt gga ctc cac cct gat gtt gtt acc ttc acc acc ctt ctc cac gga	480		
Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly			
145	150	155	160
ttg tgt gtg gaa aat agg ggt tct gaa gct ttg aat ttg ttt cat caa	528		
Leu Cys Val Glu Asn Arg Gly Ser Glu Ala Leu Asn Leu Phe His Gln			
165	170	175	
atg ttt gaa acg rca tgt agg ccc aat gtc gta acc ttc acc act ttg	576		
Met Phe Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu			
180	185	190	
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Met Asn Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu			
195	200	205	
ctt gat cgg atg atg gaa gat ggt ctc cag cct acc cag att act tat	672		
Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr			
210	215	220	
gga aca atc gta gat ggg atg tgt aag aag gga gat act gtg tct gca	720		
Gly Thr Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala			
225	230	235	240
ctg aat ctg ctg agg aag atg gag gag gtg agc cac atc ata ccc aat	768		
Leu Asn Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn			
245	250	255	
gtt gta atc tat agt gca atc att gat agc ctt tgt aaa gac gga cgt	816		
Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg			

260	265	270	
cat agc gat tct caa aat ctt ttc act gaa atg caa gag aaa gga atc	864		
His Ser Asp Ser Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile			
275	280	285	
ttt cca gat tta ttt acc tac aac tgt atg atc aac ggg ttt tgt agc	912		
Phe Pro Asp Leu Phe Thr Tyr Asn Cys Met Ile Asn Gly Phe Cys Ser			
290	295	300	
tct ggt aga tgg atc gac gcg gag cag ttg ttg caa gaa atg tta gaa	960		
Ser Gly Arg Trp Ile Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu			
305	310	315	320
agg aag atc agc cct gat gtt gta act tat aat gct ttg atc aat gca	1008		
Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala			
325	330	335	
ttt gtc aag gaa ggc aag ttc ttt gag gct gaa gaa tta tac gat gag	1056		
Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu			
340	345	350	
atg ctt cct agg ggt ata atc cct aat aca atc aca tat agt tca atg	1104		
Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met			
355	360	365	
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370	375	380	
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Phe Tyr Leu Met Pro Thr Lys Gly Cys Ser Pro Asp Val Phe Thr Phe			
385	390	395	400
aat act ctc ata gac gga tat cgt ggg gct aag agg ata gat gat gga	1248		
Asn Thr Leu Ile Asp Gly Tyr Arg Gly Ala Lys Arg Ile Asp Asp Gly			

405	410	415	
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420	425	430	
gtt act tac aac act ctt att cac ggg ttt tgt cag gtg ggc gat ctt 1344			
Val Thr Tyr Asn Thr Leu Ile His Gly Phe Cys Gln Val Gly Asp Leu			
435	440	445	
act gct gct cta gac ctt cta cat gag atg att tct agt ggt gtg tgc 1392			
Thr Ala Ala Leu Asp Leu Leu His Glu Met Ile Ser Ser Gly Val Cys			
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cct aat gtc gtt act tgt agc act ttg ctg gat ggt ctc tgc gat aac 1440			
Pro Asn Val Val Thr Cys Ser Thr Leu Leu Asp Gly Leu Cys Asp Asn			
465	470	475	480
ggg aaa cta aaa gat gca tgg gaa ctg ttt aag gtt atg cag aag agt 1488			
Gly Lys Leu Lys Asp Ala Trp Glu Leu Phe Lys Val Met Gln Lys Ser			
485	490	495	
aag atg gat ctt gat gct agt cac ccc ttc aat ggt gtg gaa cct gat 1536			
Lys Met Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp			
500	505	510	
gtt caa act tac aat ata ttg atc agc ggc ttg atc aat gaa ggg aag 1584			
Val Gln Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys			
515	520	525	
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Phe Leu Glu Ala Glu Glu Leu Tyr Lys Glu Met Pro His Arg Gly Ile			
530	535	540	
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Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys			



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cag agc cgc ctg gat gag gct aca caa atg ttt gat tcg atg ggt agc	1728			
Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser				
565	570	575		
aag agc ttc tct cca aac gta gtg acc ttt act aca ctc att gat ggc	1776			
Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asp Gly				
580	585	590		
tac tgt aaa gca gga agg gtt gat gat ggg ctg gag ctt ttc tgc gag	1824			
Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu				
595	600	605		
atg ggt aga aga ggg ata gtt gct aat aca att act tac atc act ttg	1872			
Met Gly Arg Arg Gly Ile Val Ala Asn Thr Ile Thr Tyr Ile Thr Leu				
610	615	620		
att cgt ggt ttt cgc aat gtg ggt aat att aat ggg gct cta gac att	1920			
Ile Arg Gly Phe Arg Asn Val Gly Asn Ile Asn Gly Ala Leu Asp Ile				
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ttc cag gag atg att tca agt ggt gtg tat cct ggt atc att act atc	1968			
Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Gly Ile Ile Thr Ile				
645	650	655		
cgc agt atg ctg act ggt tta tgg agt aaa gag gaa cta aaa agg aca	2016			
Arg Ser Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Thr				
660	665	670		
gtg gca atg ctt gag gaa ctg cag atg agt gtg ggg tat cag ttg gag	2064			
Val Ala Met Leu Glu Glu Leu Gln Met Ser Val Gly Tyr Gln Leu Glu				
675	680	685		
gat gaa tga			2073	
Asp Glu Xaa				

690

<210> 19

<211> 691

<212> PRT

<213> Raphanus sativus

<400> 19

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Lys Ala Ser Arg Asp Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu

35 40 45

Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp

50 55 60

Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser

65 70 75 80

Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Lys Arg

85 90 95

Pro Asp Val Val Ile Ser Leu His Lys Lys Met Glu Met Arg Arg Ile

100 105 110

Pro Cys Asp Ala Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser

115 120 125

Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Leu Thr Lys

130 135 140

Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly

145 150 155 160

Leu Cys Val Glu Asn Arg Gly Ser Glu Ala Leu Asn Leu Phe His Gln

	165	170	175
Met Phe Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu			
	180	185	190
Met Asn Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu			
	195	200	205
Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr			
	210	215	220
Gly Thr Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala			
225	230	235	240
Leu Asn Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn			
	245	250	255
Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg			
	260	265	270
His Ser Asp Ser Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile			
	275	280	285
Phe Pro Asp Leu Phe Thr Tyr Asn Cys Met Ile Asn Gly Phe Cys Ser			
	290	295	300
Ser Gly Arg Trp Ile Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu			
305	310	315	320
Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala			
	325	330	335
Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu			
	340	345	350
Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met			
	355	360	365
Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met			
370	375	380	

Phe Tyr Leu Met Pro Thr Lys Gly Cys Ser Pro Asp Val Phe Thr Phe  
385 390 395 400  
Asn Thr Leu Ile Asp Gly Tyr Arg Gly Ala Lys Arg Ile Asp Asp Gly  
405 410 415  
Met Glu Leu Leu His Glu Met Thr Glu Ala Gly Leu Val Ala Asn Thr  
420 425 430  
Val Thr Tyr Asn Thr Leu Ile His Gly Phe Cys Gln Val Gly Asp Leu  
435 440 445  
Thr Ala Ala Leu Asp Leu Leu His Glu Met Ile Ser Ser Gly Val Cys  
450 455 460  
Pro Asn Val Val Thr Cys Ser Thr Leu Leu Asp Gly Leu Cys Asp Asn  
465 470 475 480  
Gly Lys Leu Lys Asp Ala Trp Glu Leu Phe Lys Val Met Gln Lys Ser  
485 490 495  
Lys Met Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp  
500 505 510  
Val Gln Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys  
515 520 525  
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530 535 540  
Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys  
545 550 555 560  
Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser  
565 570 575  
Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asp Gly  
580 585 590  
Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu

595                      600                      605  
 Met Gly Arg Arg Gly Ile Val Ala Asn Thr Ile Thr Tyr Ile Thr Leu  
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 Ile Arg Gly Phe Arg Asn Val Gly Asn Ile Asn Gly Ala Leu Asp Ile  
 625                      630                      635                      640  
 Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Gly Ile Ile Thr Ile  
 645                      650                      655  
 Arg Ser Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Thr  
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 Asp Glu Xaa

690

<210> 20

<211> 516

<212> DNA

<213> *Raphanus raphanistrum*

<400> 20

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aaa cag att cca tgt gat gta tac agc ttt aat att ctg ata aaa tgt 97

Lys Gln Ile Pro Cys Asp Val Tyr Ser Phe Asn Ile Leu Ile Lys Cys

20                      25                      30

ttc tgc agt tgc tct aag ctt ccc ttt gct ttg tct aca ttt ggt aag 145

Phe Cys Ser Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys

35                      40                      45

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 Ile Thr Lys Leu Gly Leu His Pro Asp Val Ala Thr Phe Asn Thr Leu  
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 ctc cac gga tta tgt ctt gat aag agg gtt tct gaa gcc ttg gat ttg 241  
 Leu His Gly Leu Cys Leu Asp Lys Arg Val Ser Glu Ala Leu Asp Leu  
 65 70 75 80  
 ttt cat caa atg ttt gaa acg aca tgt agg ccg aac atc ata acg ttt 289  
 Phe His Gln Met Phe Glu Thr Thr Cys Arg Pro Asn Ile Ile Thr Phe  
 85 90 95  
 acc acg ctg atg aac ggt ctt tgc tac gag ggt aga gtt gtc gaa gct 337  
 Thr Thr Leu Met Asn Gly Leu Cys Tyr Glu Gly Arg Val Val Glu Ala  
 100 105 110  
 gta gct ctg ctt gat cgg atg cta gaa gat ggt ctc cag cct gac cag 385  
 Val Ala Leu Leu Asp Arg Met Leu Glu Asp Gly Leu Gln Pro Asp Gln  
 115 120 125  
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 Ile Thr Tyr Gly Thr Ile Val Asp Gly Met Cys Lys Met Gly Asp Thr  
 130 135 140  
 gtg tct gca ttg aat ctt ctg agg aag atg gag gag ttg agc cac atc 481  
 Val Ser Ala Leu Asn Leu Leu Arg Lys Met Glu Glu Leu Ser His Ile  
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<210> 21

<211> 171

<212> DNA

<213> Raphanus raphanistrum

<400> 21

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Phe Cys Ser Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys  
35 40 45  
Ile Thr Lys Leu Gly Leu His Pro Asp Val Ala Thr Phe Asn Thr Leu  
50 55 60  
Leu His Gly Leu Cys Leu Asp Lys Arg Val Ser Glu Ala Leu Asp Leu  
65 70 75 80  
Phe His Gln Met Phe Glu Thr Thr Cys Arg Pro Asn Ile Ile Thr Phe  
85 90 95  
Thr Thr Leu Met Asn Gly Leu Cys Tyr Glu Gly Arg Val Val Glu Ala  
100 105 110  
Val Ala Leu Leu Asp Arg Met Leu Glu Asp Gly Leu Gln Pro Asp Gln  
115 120 125  
Ile Thr Tyr Gly Thr Ile Val Asp Gly Met Cys Lys Met Gly Asp Thr  
130 135 140  
Val Ser Ala Leu Asn Leu Leu Arg Lys Met Glu Glu Leu Ser His Ile  
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<210> 22

<211> 2073

<212> DNA

<213> Raphanus

<400> 22

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<210> 23

<211> 2073

<212> DNA

<213> Raphanus

<400> 23

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aagmtcacca agcttgact ccacctgat gttgttacct tcaccacct ketccaygga 480  
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<212> DNA

<213> Raphanus

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<221> Xaa

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<223> Glu or none

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10

15

Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala

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Lys Ala Ser Xaa Xaa Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu			
35	40	45	
Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp			
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Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser			
65	70	75	80
Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Xaa Arg			
85	90	95	
Pro Asp Xaa Val Ile Ser Leu Xaa Xaa Lys Met Glu Xaa Xaa Xaa Ile			
100	105	110	
Xaa Cys Asp Xaa Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser			
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Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Xaa Thr Lys			
130	135	140	
Leu Gly Leu His Pro Asp Val Xaa Thr Phe Xaa Thr Leu Leu His Gly			
145	150	155	160
Leu Cys Xaa Xaa Xaa Arg Xaa Ser Glu Ala Leu Xaa Xaa Phe His Gln			
165	170	175	
Met Phe Glu Thr Thr Cys Arg Pro Asn Xaa Xaa Thr Phe Thr Thr Leu			
180	185	190	
Met Asn Gly Leu Cys Xaa Glu Gly Arg Xaa Val Glu Ala Val Ala Leu			
195	200	205	
Leu Asp Arg Met Xaa Glu Asp Gly Leu Gln Pro Xaa Gln Ile Thr Tyr			
210	215	220	
Gly Thr Ile Val Asp Gly Met Cys Lys Xaa Gly Asp Thr Val Ser Ala			
225	230	235	240

Leu Asn Leu Leu Arg Lys Met Glu Glu Xaa Ser His Ile Xaa Pro Asn  
 245 250 255  
 Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg  
 260 265 270  
 His Ser Asp Xaa Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile  
 275 280 285  
 Phe Pro Asp Leu Phe Thr Tyr Asn Xaa Met Ile Xaa Gly Phe Cys Ser  
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 Ser Gly Arg Trp Xaa Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu  
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 Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala  
 325 330 335  
 Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu  
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 Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met  
 370 375 380  
 Phe Tyr Leu Met Xaa Thr Lys Gly Cys Ser Pro Xaa Xaa Xaa Thr Phe  
 385 390 395 400  
 Asn Thr Leu Ile Asp Gly Tyr Xaa Gly Ala Lys Arg Ile Asp Asp Gly  
 405 410 415  
 Met Glu Leu Leu His Glu Met Thr Glu Xaa Gly Leu Val Ala Xaa Thr  
 420 425 430  
 Xaa Thr Tyr Asn Thr Leu Ile His Gly Phe Xaa Xaa Val Gly Asp Leu  
 435 440 445  
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Gly Lys Leu Lys Asp Ala Xaa Glu Xaa Phe Lys Val Met Gln Lys Ser			
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Lys Xaa Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp			
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Val Gln Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys			
515	520	525	
Phe Leu Glu Ala Glu Glu Leu Tyr Xaa Glu Met Pro His Arg Gly Ile			
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Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys			
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Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser			
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Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Xaa Gly			
580	585	590	
Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu			
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Met Gly Arg Arg Gly Ile Val Ala Asn Xaa Ile Thr Tyr Ile Thr Leu			
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Ile Xaa Gly Phe Arg Xaa Val Gly Asn Ile Asn Gly Ala Leu Asp Ile			
625	630	635	640
Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Xaa Xaa Ile Thr Ile			
645	650	655	
Arg Xaa Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Xaa			
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685

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Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala

20 25 30

Lys Ala Ser Xaa Xaa Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu

35 40 45

Ser Leu Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp  
 50 55 60  
 Ala Ile Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser  
 65 70 75 80  
 Val Val Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Xaa Arg  
 85 90 95  
 Pro Asp Xaa Val Ile Ser Leu Xaa Xaa Lys Met Glu Xaa Xaa Xaa Ile  
 100 105 110  
 Xaa Cys Asp Xaa Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser  
 115 120 125  
 Cys Ser Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Xaa Thr Lys  
 130 135 140  
 Leu Gly Leu His Pro Asp Val Val Thr Phe Thr Thr Leu Leu His Gly  
 145 150 155 160  
 Leu Cys Val Glu Xaa Arg Xaa Ser Glu Ala Leu Xaa Xaa Phe His Gln  
 165 170 175  
 Met Phe Glu Thr Thr Cys Arg Pro Asn Val Val Thr Phe Thr Thr Leu  
 180 185 190  
 Met Asn Gly Leu Cys Arg Glu Gly Arg Ile Val Glu Ala Val Ala Leu  
 195 200 205  
 Leu Asp Arg Met Met Glu Asp Gly Leu Gln Pro Thr Gln Ile Thr Tyr  
 210 215 220  
 Gly Thr Ile Val Asp Gly Met Cys Lys Lys Gly Asp Thr Val Ser Ala  
 225 230 235 240  
 Leu Asn Leu Leu Arg Lys Met Glu Glu Val Ser His Ile Ile Pro Asn  
 245 250 255  
 Val Val Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg



	260	265	270
His Ser Asp Xaa Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile			
275	280	285	
Phe Pro Asp Leu Phe Thr Tyr Asn Xaa Met Ile Xaa Gly Phe Cys Ser			
290	295	300	
Ser Gly Arg Trp Xaa Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu			
305	310	315	320
Arg Lys Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala			
325	330	335	
Phe Val Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu			
340	345	350	
Met Leu Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met			
355	360	365	
Ile Asp Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met			
370	375	380	
Phe Tyr Leu Met Xaa Thr Lys Gly Cys Ser Pro Xaa Xaa Xaa Thr Phe			
385	390	395	400
Asn Thr Leu Ile Asp Gly Tyr Xaa Gly Ala Lys Arg Ile Asp Asp Gly			
405	410	415	
Met Glu Leu Leu His Glu Met Thr Glu Xaa Gly Leu Val Ala Xaa Thr			
420	425	430	
Xaa Thr Tyr Asn Thr Leu Ile His Gly Phe Xaa Xaa Val Gly Asp Leu			
435	440	445	
Xaa Ala Ala Leu Asp Leu Leu Xaa Glu Met Ile Ser Ser Gly Xaa Cys			
450	455	460	
Pro Xaa Xaa Val Thr Cys Xaa Thr Leu Leu Asp Gly Leu Cys Asp Asn			
465	470	475	480

Gly Lys Leu Lys Asp Ala Xaa Glu Xaa Phe Lys Val Met Gln Lys Ser			
485	490	495	
Lys Xaa Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp			
500	505	510	
Val Gln Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys			
515	520	525	
Phe Leu Glu Ala Glu Glu Leu Tyr Xaa Glu Met Pro His Arg Gly Ile			
530	535	540	
Val Pro Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys			
545	550	555	560
Gln Ser Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser			
565	570	575	
Lys Ser Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Xaa Gly			
580	585	590	
Tyr Cys Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu			
595	600	605	
Met Gly Arg Arg Gly Ile Val Ala Asn Xaa Ile Thr Tyr Ile Thr Leu			
610	615	620	
Ile Xaa Gly Phe Arg Xaa Val Gly Asn Ile Asn Gly Ala Leu Asp Ile			
625	630	635	640
Phe Gln Glu Met Ile Ser Ser Gly Val Tyr Pro Xaa Xaa Ile Thr Ile			
645	650	655	
Arg Xaa Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Xaa			
660	665	670	
Val Ala Met Leu Glu Xaa Leu Gln Met Ser Xaa Xaa Xaa Xaa Xaa Xaa			
675	680	685	
Xaa Xaa			

690

<210> 28  
<211> 687  
<212> PRT  
<213> Raphanus  
<220>  
<221> Xaa  
<222> 111  
<223> Arg or Pro  
<221> Xaa  
<222> 114  
<222> Ile or Val  
<221> Xaa  
<222> 140  
<223> Leu or Ile  
<221> Xaa  
<222> 150  
<223> Val or Ala  
<221> Xaa  
<222> 153  
<223> Thr or Asn  
<221> Xaa  
<222> 161  
<223> Val or Leu  
<221> Xaa  
<222> 162  
<223> Glu or Asp

<221> Xaa  
<222> 163  
<223> Asp or Lys  
<221> Xaa  
<222> 170  
<223> Asn or Asp  
<221> Xaa  
<222> 171  
<223> Leu or Phe  
<221> Xaa  
<222> 184  
<223> Val or Ile  
<221> Xaa  
<222> 185  
<223> Val or Ile  
<221> Xaa  
<222> 196  
<223> Arg or Tyr  
<221> Xaa  
<222> 200  
<223> Ile or Val  
<221> Xaa  
<222> 211  
<223> Met or Leu  
<221> Xaa  
<222> 218  
<223> Thr or Asp

<221> Xaa

<222> 232

<223> Lys or Met

<221> Xaa

<222> 248

<223> Val or Leu

<221> Xaa

<222> 252

<223> Ile or Lys

<400> 28

Met Leu Ala Arg Val Cys Gly Phe Lys Cys Ser Ser Ser Pro Ala Glu

1 5 10 15

Ser Ala Ala Arg Leu Phe Cys Thr Arg Ser Ile Arg Asp Thr Leu Ala

20 25 30

Lys Ala Ser Gly Glu Ser Cys Glu Ala Gly Phe Gly Gly Glu Ser Leu

35 40 45

Lys Leu Gln Ser Gly Phe His Glu Ile Lys Gly Leu Glu Asp Ala Ile

50 55 60

Asp Leu Phe Ser Asp Met Leu Arg Ser Arg Pro Leu Pro Ser Val Val

65 70 75 80

Asp Phe Cys Lys Leu Met Gly Val Val Val Arg Met Glu Arg Pro Asp

85 90 95

Leu Val Ile Ser Leu Tyr Gln Lys Met Glu Arg Lys Gln Ile Xaa Cys

100 105 110

Asp Xaa Tyr Ser Phe Asn Ile Leu Ile Lys Cys Phe Cys Ser Cys Ser

115 120 125

Lys Leu Pro Phe Ala Leu Ser Thr Phe Gly Lys Xaa Thr Lys Leu Gly

130	135	140	
Leu His Pro Asp Val Xaa Thr Phe Xaa Thr Leu Leu His Gly Leu Cys			
145	150	155	160
Xaa Xaa Xaa Arg Val Ser Glu Ala Leu Xaa Xaa Phe His Gln Met Phe			
	165	170	175
Glu Thr Thr Cys Arg Pro Asn Xaa Xaa Thr Phe Thr Thr Leu Met Asn			
	180	185	190
Gly Leu Cys Xaa Glu Gly Arg Xaa Val Glu Ala Val Ala Leu Leu Asp			
	195	200	205
Arg Met Xaa Glu Asp Gly Leu Gln Pro Xaa Gln Ile Thr Tyr Gly Thr			
	210	215	220
Ile Val Asp Gly Met Cys Lys Xaa Gly Asp Thr Val Ser Ala Leu Asn			
225	230	235	240
Leu Leu Arg Lys Met Glu Glu Xaa Ser His Ile Xaa Pro Asn Val Val			
	245	250	255
Ile Tyr Ser Ala Ile Ile Asp Ser Leu Cys Lys Asp Gly Arg His Ser			
	260	265	270
Asp Ala Gln Asn Leu Phe Thr Glu Met Gln Glu Lys Gly Ile Phe Pro			
	275	280	285
Asp Leu Phe Thr Tyr Asn Ser Met Ile Val Gly Phe Cys Ser Ser Gly			
	290	295	300
Arg Trp Ser Asp Ala Glu Gln Leu Leu Gln Glu Met Leu Glu Arg Lys			
305	310	315	320
Ile Ser Pro Asp Val Val Thr Tyr Asn Ala Leu Ile Asn Ala Phe Val			
	325	330	335
Lys Glu Gly Lys Phe Phe Glu Ala Glu Glu Leu Tyr Asp Glu Met Leu			
	340	345	350

Pro Arg Gly Ile Ile Pro Asn Thr Ile Thr Tyr Ser Ser Met Ile Asp			
355	360	365	
Gly Phe Cys Lys Gln Asn Arg Leu Asp Ala Ala Glu His Met Phe Tyr			
370	375	380	
Leu Met Ala Thr Lys Gly Cys Ser Pro Asn Leu Ile Thr Phe Asn Thr			
385	390	395	400
Leu Ile Asp Gly Tyr Cys Gly Ala Lys Arg Ile Asp Asp Gly Met Glu			
405	410	415	
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr			
420	425	430	
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala			
435	440	445	
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp			
450	455	460	
Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys			
465	470	475	480
Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys			
485	490	495	
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln			
500	505	510	
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu			
515	520	525	
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro			
530	535	540	
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser			
545	550	555	560
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser			

	565		570		575										
Phe	Ser	Pro	Asn	Val	Val	Thr	Phe	Thr	Thr	Leu	Ile	Asn	Gly	Tyr	Cys
	580		585		590										
Lys	Ala	Gly	Arg	Val	Asp	Asp	Gly	Leu	Glu	Leu	Phe	Cys	Glu	Met	Gly
	595		600		605										
Arg	Arg	Gly	Ile	Val	Ala	Asn	Ala	Ile	Thr	Tyr	Ile	Thr	Leu	Ile	Cys
	610		615		620										
Gly	Phe	Arg	Lys	Val	Gly	Asn	Ile	Asn	Gly	Ala	Leu	Asp	Ile	Phe	Gln
	625		630		635										
Glu	Met	Ile	Ser	Ser	Gly	Val	Tyr	Pro	Asp	Thr	Ile	Thr	Ile	Arg	Asn
	645		650		655										
Met	Leu	Thr	Gly	Leu	Trp	Ser	Lys	Glu	Glu	Leu	Lys	Arg	Ala	Val	Ala
	660		665		670										
Met	Leu	Glu	Lys	Leu	Gln	Met	Ser	Met	Asp	Leu	Ser	Phe	Gly	Gly	
	675		680		685										

<210> 29

<211> 687

<212> PRT

<213> Raphanus

<220>

<221> Xaa

<222> 140

<223> Leu or Ile

<221> Xaa

<222> 170

<223> Asn or Asp

<221> Xaa



<222> 171

<223> Leu or Phe

<400> 29

Met	Leu	Ala	Arg	Val	Cys	Gly	Phe	Lys	Cys	Ser	Ser	Ser	Pro	Ala	Glu
1				5					10					15	
Ser	Ala	Ala	Arg	Leu	Phe	Cys	Thr	Arg	Ser	Ile	Arg	Asp	Thr	Leu	Ala
			20					25					30		
Lys	Ala	Ser	Gly	Glu	Ser	Cys	Glu	Ala	Gly	Phe	Gly	Gly	Glu	Ser	Leu
			35					40					45		
Lys	Leu	Gln	Ser	Gly	Phe	His	Glu	Ile	Lys	Gly	Leu	Glu	Asp	Ala	Ile
			50					55					60		
Asp	Leu	Phe	Ser	Asp	Met	Leu	Arg	Ser	Arg	Pro	Leu	Pro	Ser	Val	Val
			65					70					75		80
Asp	Phe	Cys	Lys	Leu	Met	Gly	Val	Val	Val	Arg	Met	Glu	Arg	Pro	Asp
				85						90				95	
Leu	Val	Ile	Ser	Leu	Tyr	Gln	Lys	Met	Glu	Arg	Lys	Gln	Ile	Arg	Cys
				100						105				110	
Asp	Ile	Tyr	Ser	Phe	Asn	Ile	Leu	Ile	Lys	Cys	Phe	Cys	Ser	Cys	Ser
			115							120				125	
Lys	Leu	Pro	Phe	Ala	Leu	Ser	Thr	Phe	Gly	Lys	Xaa	Thr	Lys	Leu	Gly
			130							135				140	
Leu	His	Pro	Asp	Val	Val	Thr	Phe	Thr	Thr	Leu	Leu	His	Gly	Leu	Cys
			145							150				155	160
Val	Glu	Asp	Arg	Val	Ser	Glu	Ala	Leu	Xaa	Xaa	Phe	His	Gln	Met	Phe
				165						170				175	
Glu	Thr	Thr	Cys	Arg	Pro	Asn	Val	Val	Thr	Phe	Thr	Thr	Leu	Met	Asn
				180						185				190	

Gly	Leu	Cys	Arg	Glu	Gly	Arg	Ile	Val	Glu	Ala	Val	Ala	Leu	Leu	Asp
195				200				205							
Arg	Met	Met	Glu	Asp	Gly	Leu	Gln	Pro	Thr	Gln	Ile	Thr	Tyr	Gly	Thr
210				215				220							
Ile	Val	Asp	Gly	Met	Cys	Lys	Lys	Gly	Asp	Thr	Val	Ser	Ala	Leu	Asn
225				230				235				240			
Leu	Leu	Arg	Lys	Met	Glu	Glu	Val	Ser	His	Ile	Ile	Pro	Asn	Val	Val
245				250				255							
Ile	Tyr	Ser	Ala	Ile	Ile	Asp	Ser	Leu	Cys	Lys	Asp	Gly	Arg	His	Ser
260				265				270							
Asp	Ala	Gln	Asn	Leu	Phe	Thr	Glu	Met	Gln	Glu	Lys	Gly	Ile	Phe	Pro
275				280				285							
Asp	Leu	Phe	Thr	Tyr	Asn	Ser	Met	Ile	Val	Gly	Phe	Cys	Ser	Ser	Gly
290				295				300							
Arg	Trp	Ser	Asp	Ala	Glu	Gln	Leu	Leu	Gln	Glu	Met	Leu	Glu	Arg	Lys
305				310				315				320			
Ile	Ser	Pro	Asp	Val	Val	Thr	Tyr	Asn	Ala	Leu	Ile	Asn	Ala	Phe	Val
325				330				335							
Lys	Glu	Gly	Lys	Phe	Phe	Glu	Ala	Glu	Glu	Leu	Tyr	Asp	Glu	Met	Leu
340				345				350							
Pro	Arg	Gly	Ile	Ile	Pro	Asn	Thr	Ile	Thr	Tyr	Ser	Ser	Met	Ile	Asp
355				360				365							
Gly	Phe	Cys	Lys	Gln	Asn	Arg	Leu	Asp	Ala	Ala	Glu	His	Met	Phe	Tyr
370				375				380							
Leu	Met	Ala	Thr	Lys	Gly	Cys	Ser	Pro	Asn	Leu	Ile	Thr	Phe	Asn	Thr
385				390				395				400			
Leu	Ile	Asp	Gly	Tyr	Cys	Gly	Ala	Lys	Arg	Ile	Asp	Asp	Gly	Met	Glu

	405	410	415
Leu Leu His Glu Met Thr Glu Thr Gly Leu Val Ala Asp Thr Thr Thr			
	420	425	430
Tyr Asn Thr Leu Ile His Gly Phe Tyr Leu Val Gly Asp Leu Asn Ala			
	435	440	445
Ala Leu Asp Leu Leu Gln Glu Met Ile Ser Ser Gly Leu Cys Pro Asp			
	450	455	460
Ile Val Thr Cys Asp Thr Leu Leu Asp Gly Leu Cys Asp Asn Gly Lys			
465	470	475	480
Leu Lys Asp Ala Leu Glu Met Phe Lys Val Met Gln Lys Ser Lys Lys			
	485	490	495
Asp Leu Asp Ala Ser His Pro Phe Asn Gly Val Glu Pro Asp Val Gln			
	500	505	510
Thr Tyr Asn Ile Leu Ile Ser Gly Leu Ile Asn Glu Gly Lys Phe Leu			
	515	520	525
Glu Ala Glu Glu Leu Tyr Glu Glu Met Pro His Arg Gly Ile Val Pro			
	530	535	540
Asp Thr Ile Thr Tyr Ser Ser Met Ile Asp Gly Leu Cys Lys Gln Ser			
545	550	555	560
Arg Leu Asp Glu Ala Thr Gln Met Phe Asp Ser Met Gly Ser Lys Ser			
	565	570	575
Phe Ser Pro Asn Val Val Thr Phe Thr Thr Leu Ile Asn Gly Tyr Cys			
	580	585	590
Lys Ala Gly Arg Val Asp Asp Gly Leu Glu Leu Phe Cys Glu Met Gly			
	595	600	605
Arg Arg Gly Ile Val Ala Asn Ala Ile Thr Tyr Ile Thr Leu Ile Cys			
610	615	620	

Gly Phe Arg Lys Val Gly Asn Ile Asn Gly Ala Leu Asp Ile Phe Gln  
 625                      630                      635                      640  
 Glu Met Ile Ser Ser Gly Val Tyr Pro Asp Thr Ile Thr Ile Arg Asn  
                          645                      650                      655  
 Met Leu Thr Gly Leu Trp Ser Lys Glu Glu Leu Lys Arg Ala Val Ala  
                          660                      665                      670  
 Met Leu Glu Lys Leu Gln Met Ser Met Asp Leu Ser Phe Gly Gly  
                          675                      680                      685

<210> 30

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 30

acataaaaat cactagatac ttgacatgga ggc                      33

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 31

aagaggagga agatggcatc acagc                      25

<210> 32

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 32

tggagtaaag aggaactaaa aagggc 26

<210> 33

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 33

cagacaatag acgcataaaa ggc 23

<210> 34

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 34

gattcctttc tcttgcatTT cag 23

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 35

atctcgtcct ttaccttctg tgg

23

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 36

gatccatgca tttgtcaagg

20

<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 37

catttgtagta gcctcatcta gg

22

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 38

gtccggagag cagcccttgg tag

23

<210> 39

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 39

tcatcgtata attcttcagc etc 23

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 40

aaagacggac gtcataccga tg 22

<210> 41

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 41

gacatgtagg cccaatgtcg t 21